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NiceProt View of TrEMBL: O48663

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General information about the entry

Entry name O48663
Primary accession number O48663
Secondary accession numbers None
Entered in TrEMBL in Release 06, June 1998
Sequence was last modified in Release 06, June 1998
Annotations were last modified in Release 22, October 2002

Name and origin of the protein

Protein name Chloroplast w6 desaturase
Synonyms None
Gene name DES6
From Chlamydomonas reinhardtii [TaxID: 3055]
Taxonomy Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

References

- 1) SEQUENCE FROM NUCLEIC ACID.
MEDLINE=98158334; PubMed=9498569; [NCBI, ExPASy, EBI, Israel, Japan]
Sato N., Fujiwara S., Kawaguchi A., Tsuzuki M.;
"Cloning of a gene for chloroplast w6 desaturase of a green alga, Chlamydomonas reinhardtii";
J. Biochem. 122:1224-1232(1997).

Comments

None

Cross-references

EMBL AB007640; BAA23881.1; - [EMBL / GenBank / DDBJ] [CodingSequence]
InterPro IPR005804: FA_desat_fam.
Graphical view of domain structure.
Pfam PF00487: FA_desaturase_1.
ProDom PD001081: FA_desat_fam:2.
[Domain structure / List of seq. sharing at least 1 domain].
ProMap O48663.
ProSAGE O48663
ModBase O48663.
SWISS-2DPAGE GET REGION ON 2D PAGE.

Keywords

None

Features

None

Sequence information

Length: 424 AA Molecular weight: 48377 Da CRC64: D553054C1CEE6B0D [This is a checksum on the sequence]

10 20 30 40 50 60

```
AFALRSPGA VRAPACAQRA SGVRAAKPGF LRSAAVARPQ VQTNAALSV PVNQLTOEER
      70      80      90     100     110     120
NLARELGK SIGRELPDNV SLTDIISKMP AEVFKLDHGK AWRACLTIA ACSACWYLIS
      130     140     150     160     170     180
SPWYLLPAA WALAGTFTG CFVIGHDCGH RSFHENNLIE DIVGHIFFAP LIYPFEPWRI
      190     200     210     220     230     240
HNHHHAHTN KLVEDTAWHP VTEADMAKWD STSAMLYKVF LGTPLKLWAS VGHVWVWHP
      250     260     270     280     290     300
NKYTPKQRT RVVISLAVVY GFMATAFPAL LYEGGPWAFV KYWLMPLWGY HFWMSTFTV
      310     320     330     340     350     360
HTAPHIPFK KAEENNAAKA QLSGTVHCDF PNWVEFLTHD ISWHVPHVA PKIPWYNLRK
      370     380     390     400     410     420
TESLRENWG QYMTCTFMW RVVKNICTEC HVDYKVNK PFDYKKEAL FAVQRRVLPD
```

cf seq id no: 11.


AAF


O48663 in FASTA format


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 Direct BLAST submission at EMBLnet-CH/SIB (Switzerland)

 Direct BLAST submission at NCBI (Bethesda, USA)

 ScanProsite, MotifScan

 Tools
Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

 Feature table viewer (Java)

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NiceProt View of TrEMBL: O53604

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General information about the entry

entry name O53604
 primary accession number O53604
 secondary accession numbers None
 entered in TrEMBL in Release 06, June 1998
 sequence was last modified in Release 06, June 1998
 annotations were last modified in Release 20, March 2002
 Name and origin of the protein
 protein name Hypothetical protein Rv0059
 synonyms None
 gene name RV0059 or MTV030.02 or MT0065
 from *Mycobacterium tuberculosis* [TaxID: 1773]
 taxonomy Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

References

1) SEQUENCE FROM NUCLEIC ACID.

STRAIN=H37Rv;

MEDLINE=98295987; PubMed=9634230; [NCBI, ExPASy, EBI, Israel, Japan]

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltham D., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean L., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrall B.G.

"Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence.";

Nature 393:537-544(1998).

2) SEQUENCE FROM NUCLEIC ACID.

STRAIN=CDC 1551 / Oshkosh;

Elischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Ueberback T., Weidman J., Khoum H., Gill J., Mikula A., Bishai W.

"Whole genome comparison of *Mycobacterium tuberculosis* clinical and laboratory strains.";

Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

Comments

None

Cross-references

EMBL AL021428; CAA16240.1; - [EMBL / GenBank / DDBJ] [CodingSequence]
 AF006919; AAK44287.1; - [EMBL / GenBank / DDBJ] [CodingSequence]
 FTR MT0065; -
 TubercuList Rv0059; -
 ProDom [Domain structure / List of seq. sharing at least 1 domain].
 ProtoMap O53604

RESAGE O53604
IodBase O53604
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Keywords

hypothetical protein; Complete proteome.

Features

one

Sequence information

Length: 230 AA Molecular weight: 25580 Da CRC64: 1A109D34B16590A8 [This is a checksum on the sequence]

10 20 30 40 50 60
| | | | | |
ITRYKPESG FVARSGGPDR KRPHDITVWH FTHADNLPGL ITAGRLADS AVTPTTEVAY

70 80 90 100 110 120
| | | | | |
PVKELRRHK WAPDSRYPA SMASDHVPFY IAARSPMLYV VCKGHSGYSG GAGPLVHLGV

130 140 150 160 170 180
| | | | | |
LGDIIADAL TWCASDGNA ASYTKFSRQV DTLGTFVDFD LLCQRQWMNT DDDPNRQSR

190 200 210 220 230
| | | | |
AEILVYGHV PFELVSYVCC YNTETMTRVR TLDPVGGVR KYVIKPGMY

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ScanProsite, MotifScan



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dollet (Java)



Feature table viewer (Java)



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